



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 147098**

**TO: Nita M Minnifield**  
**Location: rem/3c01/3c18**  
**Art Unit: 1645**  
**Thursday, March 10, 2005**  
**Case Serial Number: 10/613228**

**From: Barb O'Bryen**  
**Location: Biotech-Chem Library**  
**Remsen 1A69**  
**Phone: 571-272-2518**

**barbara.obryen@uspto.gov**

### **Search Notes**

# RUSH

*Reviewed  
3/17/05  
mm*

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 16:53:39 ; Search time 156 Seconds  
(without alignments)  
230.757 Million cell updates/sec

Title: US-10-613-228A-1

Perfect score: 22  
Sequence: 1 tcgtcggttttcgtcggtttt 22

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A-COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B-COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A-COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B-COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS-COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.2	78.2	133	4	US-09-313-294A-108
2	17.2	78.2	513	4	US-09-107-532A-292
3	16.8	76.4	36016	4	US-09-949-016-14223
4	16.4	74.5	35311	1	US-08-629-600-1
5	16.4	74.5	35311	3	US-09-076-761-1
6	16.2	73.6	909	4	US-09-134-000C-3167
7	16.2	73.6	2358	4	US-09-134-000C-3285
8	15.8	71.8	660	4	US-09-489-039A-560
9	15.6	70.9	231	4	US-09-543-681A-2772
10	15.6	70.9	300	4	US-09-543-681A-1478
11	15.6	70.9	440	4	US-09-513-998C-35185
12	15.6	70.9	599	4	US-09-270-767-3552
13	15.6	70.9	599	4	US-09-270-767-18834
14	15.6	70.9	601	4	US-09-949-016-31352
15	15.6	70.9	601	4	US-09-949-016-69221
16	15.6	70.9	601	4	US-09-949-016-81370
17	15.6	70.9	601	4	US-09-949-016-127420
18	15.6	70.9	601	4	US-09-949-016-177125
19	15.6	70.9	601	4	US-09-949-016-177126
20	15.6	70.9	601	4	US-09-949-016-177127
21	15.6	70.9	678	3	US-09-134-001C-2551
22	15.6	70.9	826	3	US-09-221-0178-1008
23	15.6	70.9	850	3	US-08-617-860B-34
24	15.6	70.9	1068	4	US-09-543-681A-2972
25	15.6	70.9	1734	4	US-09-248-796A-4704
26	15.6	70.9	2109	4	US-09-248-796A-2999
27	15.6	70.9	2394	4	US-09-540-236-893

28	15.6	70.9	3069	3	US-08-335-865J-7	Sequence 7, Appl1
29	15.6	70.9	3805	3	US-09-513-729B-10	Sequence 10, Appl1
30	15.6	70.9	3805	4	US-09-023-655-1443	Sequence 1443, Ap
31	15.6	70.9	4071	3	US-09-513-037C-5	Sequence 5, Appl1
32	15.6	70.9	4071	4	US-09-746-801A-5	Sequence 5, Appl1
33	15.6	70.9	4285	4	US-09-949-016-689	Sequence 689, App
34	15.6	70.9	4308	4	US-09-394-142B-23	Sequence 23, Appl1
35	15.6	70.9	4643	2	US-08-605-106-6	Sequence 6, Appl1
36	15.6	70.9	5061	3	US-09-355-160D-1	Sequence 1, Appl1
37	15.6	70.9	5061	4	US-10-092-219-1	Sequence 1, Appl1
38	15.6	70.9	5296	4	US-09-949-016-2362	Sequence 2362, Ap
39	15.6	70.9	8302	3	US-09-234-827B-1	Sequence 1, Appl1
40	15.6	70.9	10204	4	US-09-949-016-14104	Sequence 14104, A
41	15.6	70.9	10482	3	US-09-322-478-23	Sequence 23, Appl1
42	15.6	70.9	10482	4	US-09-586-106D-23	Sequence 23, Appl1
43	15.6	70.9	14066	4	US-09-601-198-56	Sequence 56, Appl1
44	15.6	70.9	26709	4	US-09-949-016-17520	Sequence 17520, A
45	15.6	70.9	34279	4	US-09-596-002-26	Sequence 26, Appl1

ALIGNMENTS

RESULT 1  
US-09-313-294A-108  
; Sequence 108, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Ialugudi, Raghunath V.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313,294A  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 7600  
; SOFTWARE: PERL Program  
; SEQ ID NO 108  
; LENGTH: 133  
; TYPE: DNA  
; ORGANISM: Zea mays  
; NAME/KEY: misc feature  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6476212 700548545H1  
; NAME/KEY: unsure  
; LOCATION: 8  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-313-294A-108

Query Match 78.2%; Score 17.2; DB 4; Length 133;  
Best Local Similarity 86.4%; Pred. No. 1.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCGTCGTTTTTCGTCGTTTTT 22  
||||| ||||| ||||| |||||  
Db 72 TCGTCGTTGTTTCGTCGTGTTT 93

RESULT 2  
US-09-107-532A-292/c  
; Sequence 292, Application US/09107532A  
; Patent No. 6583375  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 18:45:43 ; Search time 578 Seconds  
(without alignments)  
225.856 Million cell updates/sec

Title: US-10-613-228A-1

Perfect score: 22

Sequence: 1 tcgtcgcttttcgtcgctttt 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US05\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09C\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	17	US-10-613-228A-1
2	22	100.0	22	18	US-10-816-220-152
3	20.4	92.7	618	18	US-10-363-345A-34257
C 4	20.4	92.7	618	18	US-10-363-345A-34258
5	20.4	92.7	619	18	US-10-363-345A-40287
C 6	20.4	92.7	619	18	US-10-363-345A-40288
7	20.4	92.7	761	18	US-10-363-345A-2025
C 8	20.4	92.7	761	18	US-10-363-345A-2026
9	20.4	92.7	1024	18	US-10-363-345A-7203
C 10	20.4	92.7	1024	18	US-10-363-345A-7204
11	19.4	88.2	511	18	US-10-363-345A-28015

C 12	19.4	88.2	511	18	US-10-363-345A-28016
C 13	19.4	88.2	523	18	US-10-363-345A-35059
C 14	19.4	88.2	523	18	US-10-363-345A-35060
C 15	19.4	88.2	524	18	US-10-363-345A-40325
C 16	19.4	88.2	524	18	US-10-363-345A-40326
C 17	19.4	88.2	610	18	US-10-363-345A-23153
C 18	19.4	88.2	610	18	US-10-363-345A-23154
C 19	19.4	88.2	838	18	US-10-363-345A-32131
C 20	19.4	88.2	838	18	US-10-363-345A-32132
C 21	19.4	88.2	839	18	US-10-363-345A-1741
C 22	19.4	88.2	839	18	US-10-363-345A-1742
C 23	19.4	88.2	885	18	US-10-363-345A-18089
C 24	19.4	88.2	885	18	US-10-363-345A-18090
C 25	19.4	88.2	1267	18	US-10-363-345A-27261
C 26	19.4	88.2	1267	18	US-10-363-345A-27262
C 27	19.4	88.2	3673778	16	US-10-312-841-2
C 28	19.4	86.4	920	18	US-10-363-345A-20285
C 29	19.4	86.4	920	18	US-10-363-345A-20286
C 30	18.8	85.5	523	18	US-10-363-345A-17495
C 31	18.8	85.5	523	18	US-10-363-345A-17496
C 32	18.8	85.5	524	18	US-10-363-345A-15599
C 33	18.8	85.5	524	18	US-10-363-345A-15599
C 34	18.8	85.5	525	18	US-10-363-345A-15600
C 35	18.8	85.5	525	18	US-10-363-345A-35507
C 36	18.8	85.5	553	18	US-10-363-345A-35508
C 37	18.8	85.5	553	18	US-10-363-345A-39041
C 38	18.8	85.5	561	18	US-10-363-345A-39042
C 39	18.8	85.5	561	18	US-10-363-345A-35972
C 40	18.8	85.5	651	18	US-10-363-345A-34913
C 41	18.8	85.5	651	18	US-10-363-345A-34914
C 42	18.8	85.5	712	18	US-10-363-345A-27451
C 43	18.8	85.5	712	18	US-10-363-345A-27452
C 44	18.8	85.5	759	18	US-10-363-345A-3263
C 45	18.8	85.5	759	18	US-10-363-345A-3264

#### ALIGNMENTS

##### RESULT 1

US-10-613-228A-1  
; Sequence 1, Application US/10613228A  
; Publication No. US20040092472A1  
; GENERAL INFORMATION:  
; APPLICANT: KRIG, ARTHUR M  
; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS FOR STIMULATING IMMUNE RESPONSES  
; FILE REFERENCE: C1037.70045US00  
; CURRENT APPLICATION NUMBER: US/10/613,228A  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: US 60/394,193  
; PRIOR FILING DATE: 2002-07-03  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Oligodeoxynucleotide  
US-10-613-228A-1

Query Match 100.0%; Score 22; DB 17; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.8;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTTCGTGCGTTTTT 22

Db 1 TCGTCGTTTTTCGTGCGTTTTT 22

##### RESULT 2

US-10-816-220-152  
; Sequence 152, Application US/10816220

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 17:17:45 ; Search time 3444 Seconds  
(without alignments)  
243.152 Million cell updates/sec

Title: US-10-613-228A-1

Perfect score: 22

Sequence: 1 tgcgtgttttttcgtgcgttttt 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hrc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsl1:\*  
9: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20.4	92.7	433	BG428594	602494726
C 2	19.4	88.2	957	AG126335	Pan trogl
C 3	19.4	88.2	969	AG084147	Pan trogl
C 4	19.4	86.4	473	CN197708	TGESTZy15
C 5	18.8	85.5	698	AV895065	AV895065
C 6	18.8	85.5	750	CL653482	PR10118C
C 7	18.8	85.5	755	BP006348	BP006348
C 8	18.8	85.5	793	CL659802	PR10135b
C 9	18.8	85.5	1173	CG745933	P039-1-A0
C 10	18.8	85.5	1201	CR704325	Tetraodon
C 11	18.8	85.5	1372	CG751386	P045-4-D0
C 12	18.4	83.6	506	AV955361	AV955361
C 13	18.4	83.6	517	AV967757	AV967757
C 14	18.4	83.6	651	BW207212	BW207212
C 15	18.4	83.6	652	BW336085	BW336085
C 16	18.4	83.6	661	BW362385	BW362385
C 17	18.4	83.6	701	BP003979	BP003979
C 18	18.4	83.6	706	BW477298	BW477298
C 19	18.4	83.6	711	BW435032	BW435032
C 20	18.4	83.6	1101	CNS000Y0	AL097002
C 21	18.4	83.6	236	W66251	TGESTZy2c0
C 22	17.8	80.9	246	CB365542	CB365542
C 23	17.8	80.9	285	CN198693	TGESTZy16
C 24	17.8	80.9	342	CB353501	ZF001-P00

C 25	17.8	80.9	362	1	AV678562	AV678562
C 26	17.8	80.9	374	1	AV679629	AV679629
C 27	17.8	80.9	376	5	BW103452	BW103452
C 28	17.8	80.9	378	1	AV894777	AV894777
C 29	17.8	80.9	396	6	CB352916	2F001-P00
C 30	17.8	80.9	444	5	BW589623	BW589623
C 31	17.8	80.9	471	1	AV679587	AV679587
C 32	17.8	80.9	498	5	BW575333	BW575333
C 33	17.8	80.9	498	7	CN769410	CN769410
C 34	17.8	80.9	499	1	AV887894	AV887894
C 35	17.8	80.9	504	2	AW422790	AW422790
C 36	17.8	80.9	512	4	BG892389	BG892389
C 37	17.8	80.9	513	7	CN769717	CN769717
C 38	17.8	80.9	525	1	AV885063	AV885063
C 39	17.8	80.9	541	4	BG307575	BG307575
C 40	17.8	80.9	544	5	BW104367	BW104367
C 41	17.8	80.9	545	5	BW187581	BW187581
C 42	17.8	80.9	555	5	BQ420126	BQ420126
C 43	17.8	80.9	559	6	CB353813	CB353813
C 44	17.8	80.9	563	4	B1706183	B1706183
C 45	17.8	80.9	564	2	BE200845	BE200845

## ALIGNMENTS

RESULT 1  
BG428594/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG428594 602494726P1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4608342 5',  
433 bp mRNA linear EST 14-MAR-2001  
mrna sequence.  
BG428594  
EST.  
GI:13335100  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (Bases 1 to 433)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCMI350 row: d column: 07  
High quality sequence stop: 132.  
Location/Qualifiers  
1..433  
/organism="Homo sapiens"  
/mol\_type="mrna"  
/db\_xref="taxon:9606"  
/clones="IMAGE:4608342"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_75"  
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:  
SfiI (ggccgctcgcc); Site 2: SfiI (ggccattagcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGGCATTATGCG-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGGAGCGGCGCATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.65  
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 14:14:33 ; Search time 3888 Seconds  
(without alignments)  
274.181 Million cell updates/sec

Title: US-10-613-228A-1

Perfect score: 22

Sequence: 1 tcgtcggttttcgtcggtttt 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_ats.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.4	92.7	226153	2	AC073704 Mus muscu
2	19.4	88.2	349880	6	AX344573 Sequence
3	18.8	85.5	5826	6	AX356381 Sequence
4	18.8	85.5	6130	6	AX251400 Sequence
5	18.8	85.5	6130	6	AX345031 Sequence
6	18.8	85.5	7728	6	AX344979 Sequence
7	18.8	85.5	7728	6	AX348500 Sequence
8	18.8	85.5	8951	6	AX345897 Sequence
9	18.8	85.5	13133	6	AX344227 Sequence
10	18.4	83.6	20	6	AX104184 Sequence
11	18.4	83.6	20	6	AX355698 Sequence
12	18.4	83.6	20	6	AX547237 Sequence
13	18.4	83.6	5369	6	CQ000212 Sequence
14	18.4	83.6	146491	2	AC019950 Drosophil
15	18.4	83.6	182601	3	AC009904 Drosophil
16	18.4	83.6	236375	3	AE003708 Drosophil
17	18.4	83.6	310967	1	AE016869 Pseudomon
18	18.4	81.8	149269	2	BX897667 Danio rer
19	17.8	80.9	1527	5	BC056691 Danio rer

20	17.8	80.9	2290	3	AJ606934	Spirula s
21	17.8	80.9	2322	8	AY139885	Porphyra
22	17.8	80.9	2381	6	AX347239	Sequence
23	17.8	80.9	7195	6	AX277866	Sequence
24	17.8	80.9	7195	6	AX323551	Sequence
25	17.8	80.9	11622	6	AX345576	Sequence
26	17.8	80.9	34216	3	U57054	Sequence
27	17.8	80.9	99176	5	BX255893	Caenorhabdi
28	17.8	80.9	172585	2	CR847782	zebrafish
29	17.8	80.9	215917	2	AC006764	Danio rer
30	17.8	80.9	253250	1	AP005339	Caenorhab
31	17.8	80.9	300045	1	AE016803	Vibrio vu
32	17.8	80.9	303121	1	AE016766	Escherich
33	17.4	79.1	4110	6	AX598855	Sequence
34	17.4	79.1	5774	6	AX278031	Sequence
35	17.4	79.1	5774	6	AX323798	Sequence
36	17.4	79.1	5938	6	AX344811	Sequence
37	17.4	79.1	6067	6	AX344680	Sequence
38	17.4	79.1	6124	8	AB010408	Arabidops
39	17.4	79.1	7004	6	AX277956	Sequence
40	17.4	79.1	7004	6	AX323651	Sequence
41	17.4	79.1	7110	6	CQ006871	Sequence
42	17.4	79.1	7110	6	AX251243	Sequence
43	17.4	79.1	7110	6	AX251990	Sequence
44	17.4	79.1	7110	6	AX346458	Sequence
45	17.4	79.1	7110	6	AX349019	Sequence

## ALIGNMENTS

AC073704 226153 bp DNA linear HTG 29-JUN-2000  
Mus musculus clone RP23-175112, WORKING DRAFT SEQUENCE, 35  
unordered pieces.

AC073704  
AC073704.1 GI:8810321  
HTG; HTGS PHASE1; HTGS DRAFT.  
Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 226153)

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Center: Joint Genome Institute

Center Code: JGI

Web site: http://www.jgi.doe.gov

Project Information

Center Project Name: 1804276

Center clone name: RPCI-23\_175112

Summary Statistics

Consensus quality: 200795 bases at least Q40

Consensus quality: 211634 bases at least Q30

Consensus quality: 213977 bases at least Q20

Estimated insert size: 205410; agarose-fp estimation

Quality coverage: 7.81 in Q20 bases; agarose-fp estimation

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 35 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2005, 14:06:53 ; Search time 535 Seconds  
(without alignments)  
243.429 Million cell updates/sec

Title: US-10-613-228A-1

Perfect score: 22

Sequence: 1 tcgtcggttttcgtgcgttttt 22

Scoring table: IDENTITY\_NUC

Gapop\_10\_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	12 ADI16210	ADI16210 Immunosti
2	22	100.0	22	12 ADK19243	Adk19243 Immunosti
3	22	100.0	22	12 ADO44307	Ado44307 Nucleotid
4	20.4	92.7	618	6 ABQ47667	Abq47667 Oligonucl
5	20.4	92.7	618	6 ABQ47666	Abq47666 Oligonucl
6	20.4	92.7	619	6 ABQ53697	Abq53697 Oligonucl
7	20.4	92.7	619	6 ABQ53696	Abq53696 Oligonucl
8	20.4	92.7	761	6 ABQ15435	Abq15435 Oligonucl
9	20.4	92.7	761	6 ABQ15434	Abq15434 Oligonucl
10	20.4	92.7	1024	6 ABQ20612	Abq20612 Oligonucl
11	20.4	92.7	1024	6 ABQ20613	Abq20613 Oligonucl
12	19.4	88.2	511	6 ABQ41425	Abq41425 Oligonucl
13	19.4	88.2	511	6 ABQ41424	Abq41424 Oligonucl
14	19.4	88.2	523	6 ABQ48469	Abq48469 Oligonucl
15	19.4	88.2	523	6 ABQ48468	Abq48468 Oligonucl
16	19.4	88.2	524	6 ABQ53734	Abq53734 Oligonucl
17	19.4	88.2	524	6 ABQ53735	Abq53735 Oligonucl
18	19.4	88.2	610	6 ABQ36562	Abq36562 Oligonucl
19	19.4	88.2	610	6 ABQ36563	Abq36563 Oligonucl
20	19.4	88.2	838	6 ABQ45540	Abq45540 Oligonucl

c 21	19.4	88.2	838	6	ABQ45541	Abq45541 Oligonucl
c 22	19.4	88.2	839	6	ABQ15151	Abq15151 Oligonucl
c 23	19.4	88.2	839	6	ABQ15150	Abq15150 Oligonucl
c 24	19.4	88.2	885	6	ABQ31498	Abq31498 Oligonucl
c 25	19.4	88.2	885	6	ABQ31499	Abq31499 Oligonucl
c 26	19.4	88.2	1267	6	ABQ40670	Abq40670 Oligonucl
c 27	19.4	88.2	1267	6	ABQ40671	Abq40671 Oligonucl
c 28	19	86.4	23	12	ADK19257	Adk19257 Immunosti
c 29	19	86.4	23	12	ADK19276	Adk19276 Immunosti
c 30	19	86.4	920	6	ABQ33695	Abq33695 Oligonucl
c 31	19	86.4	920	6	ABQ33694	Abq33694 Oligonucl
c 32	18.8	85.5	523	6	ABQ30904	Abq30904 Oligonucl
c 33	18.8	85.5	523	6	ABQ30905	Abq30905 Oligonucl
c 34	18.8	85.5	524	6	ABQ29009	Abq29009 Oligonucl
c 35	18.8	85.5	524	6	ABQ29008	Abq29008 Oligonucl
c 36	18.8	85.5	525	6	ABQ48916	Abq48916 Oligonucl
c 37	18.8	85.5	525	6	ABQ48917	Abq48917 Oligonucl
c 38	18.8	85.5	553	6	ABQ52450	Abq52450 Oligonucl
c 39	18.8	85.5	553	6	ABQ52451	Abq52451 Oligonucl
c 40	18.8	85.5	561	6	ABQ49381	Abq49381 Oligonucl
c 41	18.8	85.5	561	6	ABQ49380	Abq49380 Oligonucl
c 42	18.8	85.5	651	6	ABQ48323	Abq48323 Oligonucl
c 43	18.8	85.5	651	6	ABQ48322	Abq48322 Oligonucl
c 44	18.8	85.5	712	6	ABQ40860	Abq40860 Oligonucl
c 45	18.8	85.5	712	6	ABQ40861	Abq40861 Oligonucl

ALIGNMENTS

RESULT 1

ADI16210

ID ADI16210 standard; DNA; 22 BP.

XX

AC ADI16210;

XX

DT 22-APR-2004 (first entry)

XX

DE Immunostimulatory oligodeoxynucleotide ODN 10106 SEQ ID NO:141.

XX ds; immunostimulatory; antibacterial; antiallergic; antiasthmatic;

KW cytostatic; virucide; fungicide; antiparasitic; interleukin antagonist;

KW gene therapy; infectious disease; allergy; asthma; cancer.

XX Unidentified.

XX WO2004005476-A2.

XX

PD 15-JAN-2004.

XX

PF 03-JUL-2003; 2003WO-US021113.

XX

PR 03-JUL-2002; 2002US-0393880P.

PR 03-JUL-2002; 2002US-0394090P.

PR 03-JUL-2002; 2002US-0394091P.

PR 03-JUL-2002; 2002US-0394164P.

XX

PA (COLE-) COLEY PHARM GROUP INC.

XX

PI Krieg AM;

XX

DR WPI; 2004-091353/09.

XX

PT New immunostimulatory nucleic acid molecule composition comprising CpG motifs, useful for diagnosing, preventing and/or treating infectious diseases, allergies, asthma and cancers.

XX

PS Claim 1; SEQ ID NO 141; 257pp; English.

XX

CC The invention relates to a novel composition comprising an immunostimulatory nucleic acid molecule. A composition of the invention has antibacterial, antiallergic, antiasthmatic, cytostatic, virucide,